SEQUENCE LISTING

<110> Allison, Anthony

<120> MODIFIED ANNEXIN PROTEINS AND METHODS FOR TREATING VASO-OCCLUSIVE
       SICKLE-CELL DISEASE

<130> SURR.113

<150> 60/400,718
<151> 2002-08-02

<150> 10/080,370
<151> 2002-02-21

<160> 9

<170> PatentIn version 3.2

<210> 1
<211> 960
<212> DNA
<213> Homo sapiens

<400> 1
atggccctgc gcggcaccgt gaccgacttc tccggcttcg acggccgcgc cgacgccgag   60

gtgctgcgca aggccatgaa gggcctgggc accgacgagg actccatcct gaacctgctg   120

accgcccgct ccaacgccca gcgccagcag atcgccgagg agttcaagac cctgttcggc   180

cgcgacctgg tgaacgacat gaagtccgag ctgaccggca gttcgagaa gctgatcgtg   240

gccctgatga gccctcccg cctgtacgac gcctacgagc tgaagcacgc caagctgggc   300

gccggcaccg acgagaaggt gctgaccgag atcatcgcct cccgcacccc cgaggagctg   360

cgcgccatca gcaggccta cgaggaggag tacggctcca acctggagga cgacgtggtg   420

ggcgacacct ccggctacta ccagcgcatg ctggtggtgc tgctgcaggc caaccgcgac   480

cccgacaccg ccatcgacga cgcccaggtg gagctggacg cccaggccct gttccaggcc   540

ggcgagctga agtggggcac cgacgaggag aagttcatca ccatcctggg cacccgctcc   600

gtgtcccacc tgcgccgcgt gttcgacaag tacatgacca tctccggctt ccagatcgag   660

gagaccatcg accgcgagac ctccggcaac ctggagaacc tgctgctggc cgtggtgaag   720

tccatccgct ccatccccgc ctacctggcc gagaccctgt actacgccat gaagggcgcc   780

ggcaccgacg accacaccct gatccgcgtg atcgtgtccc gctccgagat cgacctgttc   840

aacatccgca aggagttccg caagaacttc gccacctccc tgtactccat gatcaagggc   900

1

gacacctccg gcgactacaa gaaggccctg ctgctgctgt gcggcggcga ggacgactga   960

<210> 2
<211> 960
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(960)

<400> 2
atg gcc ctg cgc ggc acc gtg acc gac ttc tcc ggc ttc gac ggc cgc   48
Met Ala Leu Arg Gly Thr Val Thr Asp Phe Ser Gly Phe Asp Gly Arg
1   5   10   15

gcc gac gcc gag gtg ctg cgc aag gcc atg aag ggc ctg ggc acc gac   96
Ala Asp Ala Glu Val Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp
                20   25   30

gag gac tcc atc ctg aac ctg ctg acc gcc cgc tcc aac gcc cag cgc   144
Glu Asp Ser Ile Leu Asn Leu Leu Thr Ala Arg Ser Asn Ala Gln Arg
            35   40   45

cag cag atc gcc gag gag ttc aag acc ctg ttc ggc cgc gac ctg gtg   192
Gln Gln Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val
        50   55   60

aac gac atg aag tcc gag ctg acc ggc aag ttc gag aag ctg atc gtg   240
Asn Asp Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val
65   70   75   80

gcc ctg atg aag ccc tcc cgc ctg tac gac gcc tac gag ctg aag cac   288
Ala Leu Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His
                85   90   95

gcc aag ctg ggc gcc ggc acc gac gag aag gtg ctg acc gag atc atc   336
Ala Lys Leu Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile
                100   105   110

gcc tcc cgc acc ccc gag gag ctg cgc gcc atc aag cag gcc tac gag   384
Ala Ser Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Ala Tyr Glu
                115   120   125

gag gag tac ggc tcc aac ctg gag gac gac gtg gtg ggc gac acc tcc   432
Glu Glu Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser
        130   135   140

ggc tac tac cag cgc atg ctg gtg gtg ctg ctg cag gcc aac cgc gac   480
Gly Tyr Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg Asp
145   150   155   160

ccc gac acc gcc atc gac gac gcc cag gtg gag ctg gac gcc cag gcc   528
Pro Asp Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala

2

```
ctg ttc cag gcc ggc gag ctg aag tgg ggc acc gac gag gag aag ttc    576
Leu Phe Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe
        180             185             190

atc acc atc ctg ggc acc cgc tcc gtg tcc cac ctg cgc cgc gtg ttc    624
Ile Thr Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe
        195             200             205

gac aag tac atg acc atc tcc ggc ttc cag atc gag gag acc atc gac    672
Asp Lys Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp
    210             215             220

cgc gag acc tcc ggc aac ctg gag aac ctg ctg ctg gcc gtg gtg aag    720
Arg Glu Thr Ser Gly Asn Leu Glu Asn Leu Leu Leu Ala Val Val Lys
225             230             235             240

tcc atc cgc tcc atc ccc gcc tac ctg gcc gag acc ctg tac tac gcc    768
Ser Ile Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala
            245             250             255

atg aag ggc gcc ggc acc gac gac cac acc ctg atc cgc gtg atc gtg    816
Met Lys Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val
            260             265             270

tcc cgc tcc gag atc gac ctg ttc aac atc cgc aag gag ttc cgc aag    864
Ser Arg Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys
        275             280             285

aac ttc gcc acc tcc ctg tac tcc atg atc aag ggc gac acc tcc ggc    912
Asn Phe Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly
    290             295             300

gac tac aag aag gcc ctg ctg ctg ctg tgc ggc ggc gag gac gac tga    960
Asp Tyr Lys Lys Ala Leu Leu Leu Leu Cys Gly Gly Glu Asp Asp
305             310             315
```

<210> 3
<211> 319
<212> PRT
<213> Homo sapiens

<400> 3

```
Met Ala Leu Arg Gly Thr Val Thr Asp Phe Ser Gly Phe Asp Gly Arg
1               5               10              15

Ala Asp Ala Glu Val Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp
            20              25              30

Glu Asp Ser Ile Leu Asn Leu Leu Thr Ala Arg Ser Asn Ala Gln Arg
        35              40              45
```

```
Gln Gln Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val
    50              55              60


Asn Asp Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val
65              70              75              80


Ala Leu Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His
            85              90              95


Ala Lys Leu Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile
            100             105             110


Ala Ser Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Ala Tyr Glu
        115             120             125


Glu Glu Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser
    130             135             140


Gly Tyr Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg Asp
145             150             155             160


Pro Asp Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala
            165             170             175


Leu Phe Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe
            180             185             190


Ile Thr Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe
        195             200             205


Asp Lys Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp
    210             215             220


Arg Glu Thr Ser Gly Asn Leu Glu Asn Leu Leu Leu Ala Val Val Lys
225             230             235             240


Ser Ile Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala
            245             250             255


Met Lys Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val
            260             265             270
```

4

Ser Arg Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys
        275   280   285

Asn Phe Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly
        290   295   300

Asp Tyr Lys Lys Ala Leu Leu Leu Leu Cys Gly Gly Glu Asp Asp
305   310   315

<210> 4
<211> 2016
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<220>
<221> misc_feature
<222> (45)..(45)
<223> n = a, c, t, or g

<220>
<221> misc_feature
<222> (1000)..(1002)
<223> n = a, c, t, or g

<220>
<221> misc_feature
<222> (1051)..(1053)
<223> n = a, c, t, or g

<400> 4
atggactaca aagacgatga cgacaagctt gcggccgcga attcngccct gcgcggcacc   60

gtgaccgact tctccggctt cgacggccgc gccgacgccg aggtgctgcg caaggccatg   120

aagggcctgg gcaccgacga ggactccatc ctgaacctgc tgaccgcccg ctccaacgcc   180

cagcgccagc agatcgccga ggagttcaag accctgttcg ccgcgacct ggtgaacgac   240

atgaagtccg agctgaccgg caagttcgag aagctgatcg tggccctgat gaagccctcc   300

cgcctgtacg acgcctacga gctgaagcac gccaagctgg gcgccggcac cgacgagaag   360

gtgctgaccg agatcatcgc ctcccgcacc cccgaggagc tgcgcgccat caagcaggcc   420

tacgaggagg agtacggctc caacctggag gacgacgtgg tgggcgacac ctccggctac   480

taccagcgca tgctggtggt gctgctgcag gccaaccgcg accccgacac cgccatcgac   540

gacgcccagg tggagctgga cgcccaggcc ctgttccagg ccggcgagct gaagtggggc   600

5

```
accgacgagg agaagttcat caccatcctg ggcacccgct ccgtgtccca cctgcgccgc      660

gtgttcgaca agtacatgac catctccggc ttccagatcg aggagaccat cgaccgcgag      720

acctccggca acctggagaa cctgctgctg gccgtggtga agtccatccg ctccatcccc      780

gcctacctgg ccgagaccct gtactacgcc atgaagggcg ccggcaccga cgaccacacc      840

ctgatccgcg tgatcgtgtc ccgctccgag atcgacctgt tcaacatccg caaggagttc      900

cgcaagaact tcgccacctc cctgtactcc atgatcaagg gcgacacctc cggcgactac      960

aagaaggccc tgctgctgct gtgcggcggc gaggacgacn nnagatctcg atcgggcctg     1020

gaggtgctgt tccagggccc cggaagtact nnngccctgc gcggcaccgt gaccgacttc     1080

tccggcttcg acggccgcgc cgacgccgag gtgctgcgca aggccatgaa gggcctgggc     1140

accgacgagg actccatcct gaacctgctg accgcccgct ccaacgccca gcgccagcag     1200

atcgccgagg agttcaagac cctgttcggc cgcgacctgg tgaacgacat gaagtccgag     1260

ctgaccggca agttcgagaa gctgatcgtg gccctgatga agccctcccg cctgtacgac     1320

gcctacgagc tgaagcacgc caagctgggc gccggcaccg acgagaaggt gctgaccgag     1380

atcatcgcct cccgcacccc cgaggagctg cgcgccatca gcaggccta cgaggaggag     1440

tacggctcca acctggagga cgacgtggtg ggcgacacct ccggctacta ccagcgcatg     1500

ctggtggtgc tgctgcaggc caaccgcgac cccgacaccg ccatcgacga cgcccaggtg     1560

gagctggacg cccaggccct gttccaggcc ggcgagctga gtggggcac cgacgaggag     1620

aagttcatca ccatcctggg cacccgctcc gtgtcccacc tgcgccgcgt gttcgacaag     1680

tacatgacca tctccggctt ccagatcgag gagaccatcg accgcgagac ctccggcaac     1740

ctggagaacc tgctgctggc cgtggtgaag tccatccgct ccatccccgc ctacctggcc     1800

gagaccctgt actacgccat gaagggcgcc ggcaccgacg accacaccct gatccgcgtg     1860

atcgtgtccc gctccgagat cgacctgttc aacatccgca aggagttccg caagaacttc     1920

gccacctccc tgtactccat gatcaagggc gacacctccg cgactacaa gaaggccctg     1980

ctgctgctgt gcggcggcga ggacgactaa taataa                              2016
```

<210> 5
<211> 2016
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

6

```
<220>
<221>  CDS
<222>  (1)..(2016)

<220>
<221>  misc_feature
<222>  (45)..(45)
<223>  n = a, c, t, or g

<220>
<221>  misc_feature
<222>  (1000)..(1002)
<223>  n = a, c, t, or g

<220>
<221>  misc_feature
<222>  (1051)..(1053)
<223>  n = a, c, t, or g

<400>  5
atg gac tac aaa gac gat gac gac aag ctt gcg gcc gcg aat tcn gcc        48
Met Asp Tyr Lys Asp Asp Asp Asp Lys Leu Ala Ala Ala Asn Xaa Ala
1               5                   10                  15

ctg cgc ggc acc gtg acc gac ttc tcc ggc ttc gac ggc cgc gcc gac        96
Leu Arg Gly Thr Val Thr Asp Phe Ser Gly Phe Asp Gly Arg Ala Asp
            20                  25                  30

gcc gag gtg ctg cgc aag gcc atg aag ggc ctg ggc acc gac gag gac       144
Ala Glu Val Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Asp
        35                  40                  45

tcc atc ctg aac ctg ctg acc gcc cgc tcc aac gcc cag cgc cag cag       192
Ser Ile Leu Asn Leu Leu Thr Ala Arg Ser Asn Ala Gln Arg Gln Gln
    50                  55                  60

atc gcc gag gag ttc aag acc ctg ttc ggc cgc gac ctg gtg aac gac       240
Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val Asn Asp
65                  70                  75                  80

atg aag tcc gag ctg acc ggc aag ttc gag aag ctg atc gtg gcc ctg       288
Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu
                85                  90                  95

atg aag ccc tcc cgc ctg tac gac gcc tac gag ctg aag cac gcc aag       336
Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Lys
                100                 105                 110

ctg ggc gcc ggc acc gac gag aag gtg ctg acc gag atc atc gcc tcc       384
Leu Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile Ala Ser
            115                 120                 125

cgc acc ccc gag gag ctg cgc gcc atc aag cag gcc tac gag gag gag       432
Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Ala Tyr Glu Glu Glu
    130                 135                 140
```

7

```
tac ggc tcc aac ctg gag gac gac gtg gtg ggc gac acc tcc ggc tac          480
Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr
145             150                 155                 160

tac cag cgc atg ctg gtg gtg ctg ctg cag gcc aac cgc gac ccc gac          528
Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp
                165                 170                 175

acc gcc atc gac gac gcc cag gtg gag ctg gac gcc cag gcc ctg ttc          576
Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala Leu Phe
            180                 185                 190

cag gcc ggc gag ctg aag tgg ggc acc gac gag gag aag ttc atc acc          624
Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr
            195                 200                 205

atc ctg ggc acc cgc tcc gtg tcc cac ctg cgc cgc gtg ttc gac aag          672
Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe Asp Lys
        210                 215                 220

tac atg acc atc tcc ggc ttc cag atc gag gag acc atc gac cgc gag          720
Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu
225                 230                 235                 240

acc tcc ggc aac ctg gag aac ctg ctg ctg gcc gtg gtg aag tcc atc          768
Thr Ser Gly Asn Leu Glu Asn Leu Leu Leu Ala Val Val Lys Ser Ile
                245                 250                 255

cgc tcc atc ccc gcc tac ctg gcc gag acc ctg tac tac gcc atg aag          816
Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys
                260                 265                 270

ggc gcc ggc acc gac gac cac acc ctg atc cgc gtg atc gtg tcc cgc          864
Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val Ser Arg
            275                 280                 285

tcc gag atc gac ctg ttc aac atc cgc aag gag ttc cgc aag aac ttc          912
Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe
        290                 295                 300

gcc acc tcc ctg tac tcc atg atc aag ggc gac acc tcc ggc gac tac          960
Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr
305                 310                 315                 320

aag aag gcc ctg ctg ctg ctg tgc ggc ggc gag gac gac nnn aga tct          1008
Lys Lys Ala Leu Leu Leu Leu Cys Gly Gly Glu Asp Asp Xaa Arg Ser
                325                 330                 335

cga tcg ggc ctg gag gtg ctg ttc cag ggc ccc gga agt act nnn gcc          1056
Arg Ser Gly Leu Glu Val Leu Phe Gln Gly Pro Gly Ser Thr Xaa Ala
                340                 345                 350

ctg cgc ggc acc gtg acc gac ttc tcc ggc ttc gac ggc cgc gcc gac          1104
Leu Arg Gly Thr Val Thr Asp Phe Ser Gly Phe Asp Gly Arg Ala Asp
            355                 360                 365

gcc gag gtg ctg cgc aag gcc atg aag ggc ctg ggc acc gac gag gac          1152
```

8

```
        Ala Glu Val Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Asp
            370                 375                 380

tcc atc ctg aac ctg ctg acc gcc cgc tcc aac gcc cag cgc cag cag      1200
Ser Ile Leu Asn Leu Leu Thr Ala Arg Ser Asn Ala Gln Arg Gln Gln
385                 390                 395                 400

atc gcc gag gag ttc aag acc ctg ttc ggc cgc gac ctg gtg aac gac      1248
Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val Asn Asp
                405                 410                 415

atg aag tcc gag ctg acc ggc aag ttc gag aag ctg atc gtg gcc ctg      1296
Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu
                420                 425                 430

atg aag ccc tcc cgc ctg tac gac gcc tac gag ctg aag cac gcc aag      1344
Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Lys
                435                 440                 445

ctg ggc gcc ggc acc gac gag aag gtg ctg acc gag atc atc gcc tcc      1392
Leu Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile Ala Ser
            450                 455                 460

cgc acc ccc gag gag ctg cgc gcc atc aag cag gcc tac gag gag gag      1440
Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Ala Tyr Glu Glu Glu
465                 470                 475                 480

tac ggc tcc aac ctg gag gac gac gtg gtg ggc gac acc tcc ggc tac      1488
Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr
                485                 490                 495

tac cag cgc atg ctg gtg gtg ctg ctg cag gcc aac cgc gac ccc gac      1536
Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp
                500                 505                 510

acc gcc atc gac gac gcc cag gtg gag ctg gac gcc cag gcc ctg ttc      1584
Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala Leu Phe
                515                 520                 525

cag gcc ggc gag ctg aag tgg ggc acc gac gag gag aag ttc atc acc      1632
Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr
                530                 535                 540

atc ctg ggc acc cgc tcc gtg tcc cac ctg cgc cgc gtg ttc gac aag      1680
Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe Asp Lys
545                 550                 555                 560

tac atg acc atc tcc ggc ttc cag atc gag gag acc atc gac cgc gag      1728
Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu
                565                 570                 575

acc tcc ggc aac ctg gag aac ctg ctg ctg gcc gtg gtg aag tcc atc      1776
Thr Ser Gly Asn Leu Glu Asn Leu Leu Leu Ala Val Val Lys Ser Ile
                580                 585                 590

cgc tcc atc ccc gcc tac ctg gcc gag acc ctg tac tac gcc atg aag      1824
Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys
```

9

```
ggc gcc ggc acc gac gac cac acc ctg atc cgc gtg atc gtg tcc cgc        1872
Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val Ser Arg
    610                 615                 620

tcc gag atc gac ctg ttc aac atc cgc aag gag ttc cgc aag aac ttc        1920
Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe
625                 630                 635                 640

gcc acc tcc ctg tac tcc atg atc aag ggc gac acc tcc ggc gac tac        1968
Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr
                645                 650                 655

aag aag gcc ctg ctg ctg ctg tgc ggc ggc gag gac gac taa taa taa        2016
Lys Lys Ala Leu Leu Leu Leu Cys Gly Gly Glu Asp Asp
                660                 665
```

```
<210>  6
<211>  669
<212>  PRT
<213>  Artificial Sequence

<220>
<221>  misc_feature
<222>  (15)..(15)
<223>  The 'Xaa' at location 15 stands for Ser.

<220>
<221>  misc_feature
<222>  (334)..(334)
<223>  The 'Xaa' at location 334 stands for Lys, Asn, Arg, Ser, Thr,
       Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
       Cys, or Phe.

<220>
<221>  misc_feature
<222>  (351)..(351)
<223>  The 'Xaa' at location 351 stands for Lys, Asn, Arg, Ser, Thr,
       Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
       Cys, or Phe.

<220>
<223>  primer

<400>  6

Met Asp Tyr Lys Asp Asp Asp Asp Lys Leu Ala Ala Ala Asn Xaa Ala
1               5                   10                  15


Leu Arg Gly Thr Val Thr Asp Phe Ser Gly Phe Asp Gly Arg Ala Asp
            20                  25                  30


Ala Glu Val Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Asp
```

```
             35                      40                      45

Ser Ile Leu Asn Leu Leu Thr Ala Arg Ser Asn Ala Gln Arg Gln Gln
     50                  55                  60

Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val Asn Asp
65                  70                  75                  80

Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu
                85                  90                  95

Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Lys
            100                 105                 110

Leu Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile Ala Ser
        115                 120                 125

Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Ala Tyr Glu Glu Glu
    130                 135                 140

Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr
145                 150                 155                 160

Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp
            165                 170                 175

Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala Leu Phe
            180                 185                 190

Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr
        195                 200                 205

Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe Asp Lys
    210                 215                 220

Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu
225                 230                 235                 240

Thr Ser Gly Asn Leu Glu Asn Leu Leu Leu Ala Val Val Lys Ser Ile
            245                 250                 255

Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys
            260                 265                 270


                              11
```

```
Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val Ser Arg
        275                 280                 285


Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe
        290                 295                 300


Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr
305                 310                 315                 320


Lys Lys Ala Leu Leu Leu Leu Cys Gly Gly Glu Asp Asp Xaa Arg Ser
                325                 330                 335


Arg Ser Gly Leu Glu Val Leu Phe Gln Gly Pro Gly Ser Thr Xaa Ala
                340                 345                 350


Leu Arg Gly Thr Val Thr Asp Phe Ser Gly Phe Asp Gly Arg Ala Asp
                355                 360                 365


Ala Glu Val Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Asp
        370                 375                 380


Ser Ile Leu Asn Leu Leu Thr Ala Arg Ser Asn Ala Gln Arg Gln Gln
385                 390                 395                 400


Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val Asn Asp
                405                 410                 415


Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu
                420                 425                 430


Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Lys
                435                 440                 445


Leu Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile Ala Ser
        450                 455                 460


Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Ala Tyr Glu Glu Glu
465                 470                 475                 480


Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr
                485                 490                 495
```

12

```
Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp
        500               505            510

Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala Leu Phe
        515               520            525

Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr
        530            535               540

Ile Leu Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe Asp Lys
545            550               555               560

Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu
            565               570               575

Thr Ser Gly Asn Leu Glu Asn Leu Leu Leu Ala Val Val Lys Ser Ile
        580               585               590

Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys
        595               600               605

Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Ile Val Ser Arg
    610               615               620

Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe
625               630               635               640

Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr
            645               650               655

Lys Lys Ala Leu Leu Leu Cys Gly Gly Glu Asp Asp
        660            665
```

<210> 7
<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> primer

<220>
<221> misc_feature
<222> (1)..(30)

13

<223> primer

<400> 7
acctgagtag tcgccatggc acaggttctc   30

<210> 8
<211> 36
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 8
cccgaattca cgttagtcat cttctccaca gagcag   36

<210> 9
<211> 8
<212> PRT
<213> Artificial

<220>
<223> synthetic fusion peptide

<400> 9

Asp Tyr Lys Asp Asp Asp Asp Lys
1   5

3

S:\CLIENT FOLDERS\SURROMED\113\SEQ LISTING.TXT